

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 4, 2006, 01:49:32 ; Search time 69.1579 Seconds
(without alignments)
462.653 Million cell updates/sec

Title: US-09-701-583A-9

Perfect score: 18

Sequence: 1 cggcatgtctatttga 18

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1198766

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq:*
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq:*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*
- 9: /cgn2_6/ptodata/1/ina/backfilesi.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	3	US-08-535-249-72
2	13.8	76.7	20	3	US-09-429-322-29
3	13.4	74.4	20	3	US-10-053-662A-7
4	13.2	73.3	25	3	US-09-396-196G-19083
5	13.2	73.3	25	3	US-09-396-196G-72258
6	12.8	71.1	22	3	US-09-526-193A-254
7	12.4	68.9	20	3	US-10-393-905-35
8	12.4	68.9	20	3	US-10-660-253-21
9	12.4	68.9	24	3	US-09-460-555-3
10	12.2	67.8	18	3	US-09-422-978-11332
11	12.2	67.8	24	2	US-08-273-402B-9
12	12.2	67.8	25	3	US-09-903-013-11
13	12.2	67.8	31	2	US-08-823-516-113
14	12.2	67.8	31	3	US-08-759-038-134
15	12.2	67.8	31	3	US-08-758-314-134
16	12.2	67.8	31	3	US-09-684-938-134
17	12.2	67.8	31	3	US-09-308-825A-134
18	12.2	67.8	31	3	US-09-940-244-113
19	12.2	67.8	31	3	US-09-381-212-113
20	12.2	67.8	31	3	US-09-713-601A-113
21	12	66.7	27	3	US-09-964-994B-3
22	12	66.7	30	2	US-08-479-487-65
23	11.8	65.6	15	2	US-08-311-486C-105
24	11.8	65.6	15	2	US-08-311-486C-631

C	25	11.8	65.6	15	9	5182195-62	Patent No. 5182195
	26	11.8	65.6	19	3	US-08-475-947A-61	Sequence 61, Appl
	27	11.8	65.6	20	2	US-08-599-252-2	Sequence 2, Appl
	28	11.8	65.6	20	2	US-08-436-074-2	Sequence 2, Appl
C	29	11.8	65.6	20	3	US-09-166-186-88	Sequence 88, Appl
	30	11.8	65.6	20	3	US-09-166-186-132	Sequence 132, Appl
C	31	11.8	65.6	20	3	US-09-313-932-88	Sequence 88, Appl
	32	11.8	65.6	20	3	US-09-313-932-132	Sequence 132, Appl
C	33	11.8	65.6	20	3	US-09-313-932-453	Sequence 453, Appl
	34	11.8	65.6	20	3	US-09-887-145-43	Sequence 43, Appl
C	35	11.8	65.6	20	6	PCT-US96-06352-2	Sequence 2, Appl
	36	11.8	65.6	20	6	PCT-US96-06352-2	Sequence 2, Appl
C	37	11.8	65.6	21	3	US-09-422-978-10510	Sequence 10510, A
	38	11.8	65.6	21	3	US-09-382-552-124	Sequence 124, Appl
C	39	11.8	65.6	22	2	US-08-217-529-6	Sequence 6, Appl
	40	11.8	65.6	23	6	PCT-US93-02259-13	Sequence 13, Appl
C	41	11.8	65.6	25	3	US-09-396-196G-118255	Sequence 118255, A
	42	11.8	65.6	25	3	US-09-396-196G-118256	Sequence 118256, A
C	43	11.8	65.6	25	3	US-09-396-196G-118257	Sequence 118257, A
	44	11.8	65.6	26	3	US-09-077-734-40	Sequence 40, Appl
C	45	11.8	65.6	30	3	US-09-276-147B-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-535-249-72
; Sequence 72, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown

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;
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-08-535-249-72

Query Match      100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.3; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

Qy 1 CGGCATGCTCTATTGTGA 18
Db 1 CGGCATGCTCTATTGTGA 18

RESULT 2
US-09-429-322-29
; Sequence 29, Application US/09429322A
; Patent No. 6190869
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN KINASE C-THETA
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0100
; CURRENT APPLICATION NUMBER: US/09/429,322A
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-429-322-29

Query Match      76.7%; Score 13.8; DB 3; Length 20;
Best Local Similarity 88.2%; Pred. No. 9.7e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2;

Qy 2 GGCATGCTCTATTGTGA 18
Db 2 GGCATGCTCAATTGTGA 18

RESULT 3
US-10-053-662A-7
; Sequence 7, Application US/10053662A
; Patent No. 6916618
; GENERAL INFORMATION:
; APPLICANT: Alexandra Charlesworth
; APPLICANT: Faivia Spirito
; APPLICANT: Guerrino Meneguzzi
; APPLICANT: John Baird
; APPLICANT: Keith Linder
; TITLE OF INVENTION: ISOLATION OF THE LAMININ Y2 GENE IN
; TITLE OF INVENTION: HORSES AND ITS USE IN DIAGNOSING JUNCTIONAL EPIDERMOLYSIS
; FILE REFERENCE: P84us4
; CURRENT APPLICATION NUMBER: US/10/053,662A
; CURRENT FILING DATE: 2002-01-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
; US-10-053-662A-7

Query Match      74.4%; Score 13.4; DB 3; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.6e+03; Indels 1; Gaps 0;
Matches 14; Conservative 0; Mismatches 0;

Qy 1 CGGCATGCTCTATTGTGA 18
Db 20 CGGCATGCTCTATTGTGA 3

US-09-396-196G-19083
; Sequence 19083, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19083
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-396-196G-19083

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Best Local Similarity 83.3%; Pred. No. 2e+03; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 3;

Qy 1 CGGCATGCTCTATTGTGA 18
Db 8 CAGGATGCTCTATTGTGA 25

RESULT 5
US-09-396-196G-72258/c
; Sequence 72258, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72258
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-72258

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Best Local Similarity 83.3%; Pred. No. 2e+03; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 3;

Qy 1 CGGCATGCTCTATTGTGA 18
Db 20 CGGCATGCTCTATTGTGA 3

RESULT 6
US-09-526-193A-254/c
; Sequence 254, Application US/09526193A
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 4, 2006, 01:42:16 ; Search time 861.632 Seconds
(without alignments)
1187.494 Million cell updates/sec

Title: US-09-701-583A-9
Perfect score: 18
Sequence: 1 cggcatgtctatttga 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 1934910

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb.in.*
3: gb.env.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pr.*
9: gb.ro.*
10: gb.sts.*
11: gb.sv.*
12: gb.un.*
13: gb.vi.*
14: gb.rtg.*
15: gb.pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	18	100.0	18	6 A40535	A40535 Sequence 72
2	18	100.0	18	6 A89061	A89061 Sequence 12
3	18	100.0	18	6 BD06574	BD06574 An antisense
4	18	100.0	18	6 BD234905	BD234905 A method
5	18	100.0	18	6 CS123679	CS123679 Sequence
6	18	100.0	18	6 AR232815	AR232815 Sequence
7	18	100.0	18	6 AX008976	AX008976 Sequence
8	18	100.0	18	6 AX030110	AX030110 Sequence
9	18	100.0	18	6 AX252494	AX252494 Sequence
10	18	100.0	18	6 AX316431	AX316431 Sequence
11	18	100.0	22	6 BD234967	BD234967 A method
12	18	100.0	22	6 AX009038	AX009038 Sequence
13	18	100.0	27	6 AX113805	AX113805 Sequence
14	16	88.9	16	6 A89129	A89129 Sequence 12
15	16	88.9	16	6 BD066642	BD066642 An antisense
16	16	88.9	16	6 BD234928	BD234928 A method
17	16	88.9	16	6 AX008999	AX008999 Sequence
18	16	88.9	20	6 A88381	A88381 Sequence 52

19	16	88.9	20	6 A90348	A90348 Sequence 52
20	16	88.9	20	6 BD065894	BD065894 An antisense
21	16	88.9	20	6 BD234904	BD234904 A method
22	16	88.9	20	6 BD234965	BD234965 A method
23	16	88.9	20	6 CS123678	CS123678 Sequence
24	16	88.9	20	6 AX008975	AX008975 Sequence
25	16	88.9	20	6 AX009036	AX009036 Sequence
26	14.4	80.0	17	6 BD203421	BD203421 Method an
27	14	77.8	17	6 BD203422	BD203422 Method an
28	13.8	76.7	20	6 AR130778	AR130778 Sequence
29	13.4	74.4	30	6 CS130581	CS130581 Sequence
30	13	72.2	17	6 BD203423	BD203423 Method an
31	12.8	71.1	22	6 AR393715	AR393715 Sequence
32	12.4	68.9	20	6 AR647382	AR647382 Sequence
33	12.4	68.9	20	6 AR654435	AR654435 Sequence
34	12.4	68.9	24	6 AR321595	AR321595 Sequence
35	12.4	68.9	38	6 A35024	A35024 Synthetic P
36	12.2	67.8	18	6 AR299597	AR299597 Sequence
37	12.2	67.8	23	6 BD184058	BD184058 Method an
38	12.2	67.8	23	6 AX742234	AX742234 Sequence
39	12.2	67.8	23	6 AX798838	AX798838 Sequence
40	12.2	67.8	24	6 AR075414	AR075414 Sequence
41	12.2	67.8	24	6 BD176117	BD176117 Anticodon
42	12.2	67.8	25	6 CQ986684	CQ986684 Sequence
43	12.2	67.8	25	6 AR455613	AR455613 Sequence
44	12.2	67.8	25	6 AX353402	AX353402 Sequence
45	12.2	67.8	28	10 AL773120	AL773120 Arabidopsis

ALIGNMENTS

RESULT 1
LOCUS A40535 18 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 72 from Patent WO9425578.
ACCESSION A40535
VERSION A40535.1 GI:2296570
KEYWORDS
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS
TITLE
JOURNAL
FEATURES
source
Location/Qualifiers
1..18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
Patent: WO 9425578-A 72 10-NOV-1994;
BIOGNOSTIK GES (DE)

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCATGCTCTATTGTGA 18
| | | | | | | | | | | | | | | | | |
Db 1 CGGCATGCTCTATTGTGA 18

RESULT 2
LOCUS A89061 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1209 from Patent WO9833904.
ACCESSION A89061
VERSION A89061.1 GI:6737631
KEYWORDS unclassified
SOURCE unclassified
ORGANISM unclassified